

SEQUENCE LISTING

- (1) GENERAL INFORMATION:
- (i) APPLICANT: YEDA RESEARCH AND DEVELOPMENT CO. LTD
- (ii) TITLE OF INVENTION: RHAMNOSYL-TRANSFERASE GENE AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
- (B) STREET: 2001 Jefferson Davis Highway, Suite 207
- (C) CITY: Arlington
- (D) STATE: Virginia
- (E) COUNTRY: United States of America
- (F) ZIP: 22202
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
- (B) COMPUTER: Twinhead@ Slimnote-890TX
- (C) OPERATING SYSTEM: MS DOS version 6.2,
Windows version 3.11
- (D) SOFTWARE: Word for Windows version 2.0 converted to
an ASCII file
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Friedmam, Mark M.
- (B) REGISTRATION NUMBER: 33,883
- (C) REFERENCE/DOCKET NUMBER: 910/8
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 972-3-5625553
- (B) TELEFAX: 972-3-5625554
- (C) TELEX:
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- Asn Tyr Phe Leu His Leu Thr Ala
5 8
- (2) INFORMATION FOR SEQ ID NO:2:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
- Tyr Pro Phe
3
- (2) INFORMATION FOR SEQ ID NO:3:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
Ile Ala Ala Ile Leu Phe Leu
5 7
- (2) INFORMATION FOR SEQ ID NO:4:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
Tyr Phe Pro Ser Leu Met Gly Asn
5 8
- (2) INFORMATION FOR SEQ ID NO:5:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
Glu Lys Met Thr Ile Glu Glu Ala
5 8
- (2) INFORMATION FOR SEQ ID NO:6:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
Leu Phe Gln Pro
4
- (2) INFORMATION FOR SEQ ID NO:7:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
Val Val Asp Asn Gly Met Gly Met Val Val Pro Arg Asp Lys
5 10 14
- (2) INFORMATION FOR SEQ ID NO:8:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
GAXAAXGGIA TGGGIATGGT 20

(2) INFORMATION FOR SEQ ID NO:9:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
Asp Asn Gly Met Gly Met Val
5 7

(2) INFORMATION FOR SEQ ID NO:10:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
GAXAAXATGA CIATXGAXGA XGC 23

(2) INFORMATION FOR SEQ ID NO:11:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
AAXTAXTTXC TICAXCTIAC XGC 23

(2) INFORMATION FOR SEQ ID NO:12:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
Asn Tyr Phe Leu His Ley Thr Ala
5 8

(2) INFORMATION FOR SEQ ID NO:13:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
GTTTTCCCAG TCACGACGTT TTTTTTTTTT TTT 33

(2) INFORMATION FOR SEQ ID NO:14:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
GTTTTCCCAG TCACGACG 18

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
CATGCCCATTA CCATTGTC 18

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
GACAATGGTA TGGGCATG 18

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
CCTCAACCAC CGAGCCCCAA CCAC 24

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
CATCTAGAAT GGATACCAAG CATCAAG 27

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
CAGGATCCTT ATTCAGATTT CTTGACAAG 29

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1359
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
ATGGATACCA AGCATCAAGA TAAGCCAAGC ATTCTCATGT TACCATGGCT AGCTCATGGG 60
CACATAGCTC CACACCTTGA ACTTGCCAAG AAGCTTTCAC AGAAAACTT CCACATATAT 120
TTCTGCTCTA CTCCCAACAA TCTACAATCC TTCGGCAGAA ATGTTGAAAA AAACCTTCTCA 180
TCTTCAATAC AACTCATAGA ACTGCAACTT CCCAATACAT TCCCTGAACT TCCTTCACAA 240
AATCAGACCA CAAAAACCT TCCTCCCAT CTTATTATA CTCTCGTGGG AGCATTTGAA 300

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GACGCAAAAC CTGCTTTTTG CAACATCTTG GAGACGCTTA AACCAACCCT TGTTATGTAT 360
 GATTTGTTCC AACCGATGGC GGCGGAGGCA GCTTACCAGT ATGACATAGC TGCTATTTTG 420
 TTCTTACCCT TATCTGCAGT AGCCTGCTCT TTCTTGCTGC ACAATATCGT AAATCCCAGC 480
 CTGAAATACC CTTTCTTTGA ATCTGATTAC CAAGATAGAG AAAGCAAGAA CATCAATTAC 540
 TTCCTGCATC TTACTGCCAA TGGCACCTTA AACAAAGACA GGTTCTTAAA AGCTTTTCGAA 600
 CTATCTTGCA AATTTGTGTT CATCAAAACA TCAAGAGAGA TTGAATCCAA GTACTTGGAT 660
 TATTTTCCTT CTTTAATGGG AAATGAAATA ATTCCAGTAG GGCCTCTAAT CCAAGAACCT 720
 ACCTTCAAGG TAGATGATAC AAAGATCATG GACTGGCTGA GCCAAAAGGA GCCTCGTTCA 780
 GTCGTGTATG CATCCTTTGG CAGTGAGTAC TTTCTTCCA CGGATGAAAT ACATGACATA 840
 GCTATTGGGT TATTGCTCAC CGAGGTTAAT TTTATATGGG CTTTCAGATT ACATCCTGAT 900
 GAGAAAATGA CGATAGAGGA AGCACTGCCT CAGGGCTTTG CTGAGGAGAT TGAAAGGAAT 960
 AATAAGGGAA TGATAGTACA AGGTGGGTT CCGCAGGCTA AAATTTTAAAG GCATGGAAGC 1020
 ATCGGCGGAT TTTTGAGTCA TTGTGGTTGG GGCTCGGTGG TTGAGGGGAT GGTTTTTCGGG 1080
 GTACCAATCA TAGGTGTGCC AATGGCATAT GAGCAGCCAA GCAATGCCAA GGTGGTGGTT 1140
 GACAATGGTA TGGGCATGGT CGTTCCAAGA GATAAGATCA ATCAAAGACT TGGAGGAGAG 1200
 GAGGTGGCGA GGGTCATTAA ACATGTTGTG CTGCAAGAAG AAGCGAAGCA AATAAGAAGA 1260
 AAAGCTAATG AAATTAGTGA GAGTATGAAG AAGATAGGGG ACGCACAGAT GAGTGTGGTG 1320
 GTGGAGAAAC TGCTGCAGCT TGCAAGAAAT CTGAATAA 1359

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Asp Thr Lys His Gln Asp Lys Pro Ser Ile Leu Met Leu Pro
 5 10 15
 Trp Leu Ala His Gly His Ile Ala Pro His Leu Glu Leu Ala Lys
 20 25 30
 Lys Leu Ser Gln Lys Asn Phe His Ile Tyr Phe Cys Ser Thr Pro
 35 40 45
 Asn Asn Leu Gln Ser Phe Gly Arg Asn Val Glu Lys Asn Phe Ser
 50 55 60
 Ser Ser Ile Gln Leu Ile Glu Leu Gln Leu Pro Asn Thr Phe Pro
 65 70 75
 Glu Leu Pro Ser Gln Asn Gln Thr Thr Lys Asn Leu Pro Pro His
 80 85 90
 Leu Ile Tyr Thr Leu Val Gly Ala Phe Glu Asp Ala Lys Pro Ala
 95 100 105
 Phe Cys Asn Ile Leu Glu Thr Leu Lys Pro Thr Leu Val Met Tyr
 110 115 120
 Asp Leu Phe Gln Pro Met Ala Ala Glu Ala Ala Tyr Gln Tyr Asp
 125 130 135
 Ile Ala Ala Ile Leu Phe Leu Pro Leu Ser Ala Val Ala Cys Ser
 140 145 150
 Phe Leu Leu His Asn Ile Val Asn Pro Ser Leu Lys Tyr Pro Phe
 155 160 165
 Phe Glu Ser Asp Tyr Gln Asp Arg Glu Ser Lys Asn Ile Asn Tyr
 170 175 180
 Phe Leu His Leu Thr Ala Asn Gly Thr Leu Asn Lys Asp Arg Phe
 185 190 195
 Leu Lys Ala Phe Glu Leu Ser Cys Lys Phe Val Phe Ile Lys Thr
 200 205 210
 Ser Arg Glu Ile Glu Ser Lys Tyr Leu Asp Tyr Phe Pro Ser Leu
 215 220 225
 Met Gly Asn Glu Ile Ile Pro Val Gly Pro Leu Ile Gln Glu Pro

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230	235	240
Thr Phe Lys Val Asp Asp Thr Lys Ile	Met Asp Trp Leu Ser Gln	
245	250	255
Lys Glu Pro Arg Ser Val Val Tyr Ala	Ser Phe Gly Ser Glu Tyr	
260	265	270
Phe Pro Ser Thr Asp Glu Ile His Asp	Ile Ala Ile Gly Leu Leu	
275	280	285
Leu Thr Glu Val Asn Phe Ile Trp Ala	Phe Arg Leu His Pro Asp	
290	295	300
Glu Lys Met Thr Ile Glu Glu Ala Leu	Pro Gln Gly Phe Ala Glu	
305	310	315
Glu Ile Glu Arg Asn Asn Lys Gly Met	Ile Val Gln Gly Trp Val	
320	325	330
Pro Gln Ala Lys Ile Leu Arg His Gly	Ser Ile Gly Gly Phe Leu	
335	340	345
Ser His Cys Gly Trp Gly Ser Val Val	Glu Gly Met Val Phe Gly	
350	355	360
Val Pro Ile Ile Gly Val Pro Met Ala	Tyr Glu Gln Pro Ser Asn	
365	370	375
Ala Lys Val Val Val Asp Asn Gly Met	Gly Met Val Val Pro Arg	
380	385	390
Asp Lys Ile Asn Gln Arg Leu Gly Gly	Glu Glu Val Ala Arg Val	
395	400	405
Ile Lys His Val Val Leu Gln Glu Glu	Ala Lys Gln Ile Arg Arg	
410	415	420
Lys Ala Asn Glu Ile Ser Glu Ser Met	Lys Lys Ile Gly Asp Ala	
425	430	435
Gln Met Ser Val Val Val Glu Lys Leu	Leu Gln Leu Val Lys Lys	
440	445	450
Ser Glu		
452		